

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 4, 1999, 03:34:45 ; Search time 1417.33 Seconds

(Without alignments)
4586.373 Million cell updates/sec

Title: US-09-034-286-64

Perfect score: 1817

Sequence: 1 ACAGAGACACAGCGCTGTC.....GGAAAAAAAAAAAAAAAAAAAA 1817

Scoring table: IDENTITY_NUC

Searched: 808301 seqs, 1788773984 residues

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39: gb_ba1.*
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41: gb_pl1.*
42: gb_pl2.*
43: gb_pr3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	1491	82.1	1491	12	AF037469	AF037469 Homo sapi
5	1491	82.1	1491	36	AF043640	AF043640 Homo sapi
6	1491	82.1	1491	13	AF037469	AF037469 Homo sapi
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ALIGNMENTS

RESULT 1

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LOCUS Homo sapiens Smad6 mRNA, complete cds.

DEFINITION AF035528

ACCESSION AF035528

KEYWORDS g2736315

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2887)

AUTHORS Hata,A., Iagna,G., Massague,J. and Hemmati-Bilvanlou,A.

TITLE The Smad4 tumor suppressor

JOURNAL Genes Dev. (1997) In press

REFERENCE 2 (bases 1 to 2887)

AUTHORS Hata,A., Iagna,G., Massague,J. and Hemmati-Bilvanlou,A.

TITLE Direct Submission

JOURNAL Submitted (21-NOV-1997) Laboratory of Molecular Embryology, The Rockefeller University, 1230 York Avenue, New York, NY 10021, USA

FEATURES

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SE COUNT 509 a 899 c 929 g 349 t 1 others
ORIGIN

Query Match 97.5% Score 1772; DB 11; Length 2887;
Best Local Similarity 99.1% Pred. No. 2,4e-225;
Matches 1792; Conservative 0; Mismatches 15; Indels 1; Gaps 1;
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RESULT 2
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LOCUS Homo sapiens Smad6 mRNA, complete cds.
DEFINITION AF035528
ACCESSION 92736315
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 2887)
Hata,A., Laguna,G., Massague,J. and Hemmati-Brihanlou,A.
Smad6 inhibits BMP/Smad1 signaling by specifically competing with
the Smad6 tumor suppressor
Genes Dev. (1997) In press
2 (bases 1 to 2887)
Hata,A., Laguna,G., Massague,J. and Hemmati-Brihanlou,A.
Direct Submission
Submitted (21-NOV-1997) Laboratory of Molecular Embryology, The
Rockefeller University, 1230 York Avenue, New York, NY 10021, USA
JOURNAL
AUTHORS
TITLE
JOURNAL
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BASE COUNT 509 a 899 c 929 g 549 t
ORIGIN
1 others

Query Match 97.5% Score 1772; DB 36; Length 2887;
Best Local Similarity 99.18; Pred. No. 2.4e-225;
Matches 1792; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

QY 6 GACGACAGGCTGTGCGGCTGTGCACGCGCTCCGCGGCGAGGCTTCATGTGGGGCTGCG 65
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ORIGIN

Query Match 82.1%; Score 1491; DB 11; Length 1491;
Best Local Similarity 100.0%; Pred. No. 3.1e-188;
Matches 1491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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NID AF043640
KEYWORDS g2828711
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1491)
AUTHORS :Moren A.
TITLE Direct Submission
JOURNAL Submitted (20-JAN-1998) Ludwig Institute for Cancer Research, Box 595, Uppsala 751 24, Sweden
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RESULT 4
AF037469 1491 bp mRNA PRI 02-DEC-1998
LOCUS Homo sapiens Smad6 (Smad6) mRNA, complete cds.
DEFINITION AF037469
ACCESSION 93941317
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
Hagiwara, K., Freeman, A.H., McMenamin, M.G., Bennett, W.P.,
Nakashima, M., Minter, A.R., Yang, K., Takenoshita, S. and Harris, C.C.
Direct Submission
Submitted (09-DEC-1997) LHC, NIC, Building 37, Room 2C22 37 Convent
Drive, Bethesda, MD 20892, USA
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BASE COUNT 213 a 546 c 523 g 209 t
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Matches 1491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6

AF037469 1491 bp mRNA PRI 02-DEC-1998
LOCUS Homo sapiens Smad6 (Smad6) mRNA, complete cds.
DEFINITION AF037469
ACCESSION 93941317
NID
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
1 (bases 1 to 1491) Primates; Catarrhini; Homnidae; Homo.
Nagashima, M., Munter, A.R., Yang, K., Takenoshita, S. and Harris, C.C.
TITLE Direct Submission
JOURNAL Submitted (09-DEC-1997) IHC, NIC, Building 37, Room 2C22 37 Convent
Drive, Bethesda, MD 20892, USA

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BASE COUNT 213 a 546 c 523 g 209 t
ORIGIN

Query Match 82.1%; Score 1491; DB 43; Length 1491;
Best Local Similarity 100.0%; Pred. No. 3, 1e-188;
Matches 1491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
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 VERSION AF010133
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 SOURCE house mouse.
 ORGANISM Mus musculus
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 Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1488)
 AUTHORS Imanura, T., Takase, M., Nishihara, A., Oeda, E., Hanai, J.-I.,
 Kawabata, M., and Miyazono, K.
 TITLE Smad6 inhibits signalling by the TGF-beta superfamily
 JOURNAL Nature 389 (6651), 622-626 (1997)
 MEDLINE 97474481
 REFERENCE 2 (bases 1 to 1488)
 AUTHORS Takase, M., Kawabata, M., and Miyazono, K.
 TITLE Direct Submission
 JOURNAL Submitted (23-JUN-1997) Biochemistry, The Cancer Institute of
 Tokyo, 1-37-1 Kami-Ikebukuro, Toshima-ku, Tokyo 170, Japan
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LOCUS Human chromosome 15 Mad homolog Smad6 mRNA, complete cds.
DEFINITION U59914
ACCESSION g1554326
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ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
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REFERENCE 1 (bases 1 to 1280)
Riggins,G.J., Thisagalingam,S., Rozenblum,E., Weinstein,C.L.,
Kern,S.E., Hamilton,S.R., Willson,J.K., Markowitz,S.D.,
Kinzler,K.W. and Vogelstein,B.
Mad-related genes in the human
Nature Genet. 13 (3), 347-349 (1996)
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MEDLINE 2 (bases 1 to 1280)
Riggins,G.J., Thisagalingam,S., Kinzler,K.W. and Vogelstein,B.V.
Submitted (04-JUN-1996) Oncology Center, Rm. 109, Johns Hopkins,
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LOCUS Xenopus laevis Smad6 (Smad6) mRNA, complete cds.
DEFINITION AF041839
ACCESSION g3399770
KEYWORDS
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Vertebrata; Amphibia; Batrachia;
Anura; Mesobatrachia; Pipridae; Pipridae; Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 2051)
Nakayama,T., Gardner,H., Berg,L.K. and Christian,J.L.
Smad6 functions as an intracellular antagonist of some TGF-beta
family members during Xenopus embryogenesis
Genes Cells 3 (6), 387-394 (1998)
98403853
MEDLINE 2 (bases 1 to 2051)
Nakayama,T., Gardner,H. and Christian,J.L.
Submitted (07-JAN-1998) Department of Cell and Developmental
Biology, Oregon Health Sciences University, 3181 SW Sam Jackson
Park Road, Portland, OR 97201-3098, USA
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Location/Qualifiers
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AF035529	DEFINITION	Xenopus Smad6 mRNA, partial cds.			
AF035529	ACCESSION				
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SOURCE		African clawed frog.			
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REFERENCE		1 (bases 1 to 848)			
AUTHORS		Hata,A., Iagna,G., Massague,J. and Hemmati-Briylanlou,A.			
TITLE		Smad6 inhibits BMP/Smad1 signaling by specifically competing with			
JOURNAL		the Smad4 tumor suppressor			
REFERENCE		Genes Dev. (1997) In press			
AUTHORS		2 (bases 1 to 848)			
TITLE		Hata,A., Iagna,G., Massague,J. and Hemmati-Briylanlou,A.			
JOURNAL		Direct Submission			
REFERENCE		Submitted (21-Nov-1997) Laboratory of Molecular Embryology, The			
AUTHORS		Rockefeller University, 1230 York Avenue, New York, NY 10021, USA			
JOURNAL		Location/Qualifiers			
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Page 12

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31-JUL-1998

ANISM Mus musculus

Characterization of a novel mouse homologue of Mediator TCE-10

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	1877	6CAGCCGCCCTCGTCTACTCGCTCCCCCTCCTGCTGTGCAAAAGTGTTCAGTGGCCGGA	1936
Db	1877	6CAGCCGCCCTCGTCTACTCGCTCCCCCTCCTGCTGTGCAAAAGTGTTCAGTGGCCGGA	1936
QY	856	CTGCAAGCAGCGCGGTGAGAGTGAAGCCCTGTGCGGTGCGCAGACTTGGCCGCCGCGC	915
Db	1937	TCGTCAGGCATTCCTGGAAAGTCAAGAGGCTGTGTTGCTGTGAATCTTACGGGAAGATCA	1996
QY	916	CGACGGCCCTACCGTGTGTGCAACCCCTTACACATTCAAGCGGGCTCTGCGGGCCGAATC	975
Db	1997	CCCCGAGC---TGTGTGTGTGCAACCCCATCATCCTTATCACTCTGTGAACATGAGATC	2053
QY	976	TCCGCCACATCCCTACTCTGTGCGGTGTCTCTCTGCGAGAGTACGAAGCCAGCTGATCTTC	1035
Db	2054	TCCCCCTCTCTCTACTCTCCAGATACCAATGGATTTTCTCAAAACCAATGCAAGCTGTCC	2113
QY	1036	CGATTCCATCTTCTCTTACACTGAAGCGAGGTACCACTCCATCATCTGTCCGG	1095
Db	2114	AGATGTGTGATCTCTCCCGCGGAACCGGGGAAGAGATTTATCT-----GGCCCCG	2167
QY	1096	TGAATTTCTACAGCCGACGATGTCTCCGAGCGCCACCAAGCCGAGCCACTGTGTGACGT	1155
Db	2168	GGGGCTTTTCAGATTTCCCACTTCTTGAGAGCTGTGGATTCGCTCACTGTGTGTGTGT	2227
QY	1156	GGGCTACTGGAGACACCGAGCGCGGTGGGGCCGCTCTATGGGGTGTACGACAGCGGT	1215
Db	2228	GGCACTATGGAGAGAGAGACTGCGTGGGAGAGCTCTACTGTGTCCAGAGACCTCCCT	2287
QY	1216	CAGACTTTTATGACCTTACTTACGAGGAGCGGCTCTGCTGTGGGCACTCAACCTGGA	1279
Db	2288	GGATATTTTATGATTAATCTACTCTAGGGGAATGAGCTTTGCTGTGGAAGCTAATTCGA	2347
QY	1276	GCAAGCGAGCGAGTGGTGGTGGCGGAACGCGCAGCAAGATGGCTTGGCATCTGTGAG	1335
Db	2348	CAACAAAGATGACGTGGTATCAGAAAGTGGGAGCAGATCGGCTGTGGCATCAAGTGC	2407
QY	1336	CAGAGAGCCGAGCGGTGTGGGCTCTACAAACCGCGGAGAGACCCCATTTGTCAATCT	1395
Db	2408	GCGGGAAGTGAATGGCTGTGGGTTTACCAACGCGACAGATTACCCCATTTATCAAGTC	2467
QY	1396	CCGACAGCTGAGCGCGCCGCGCGCGCTGTGTGTGTGCGCAAGGTCCCCCGGCTA	1455
Db	2468	CGCCACACTGACACACCCGAGATCTCAGAGAGCTGTGTGTGTGACAAAGTCTTCCGTGTT	2527
QY	1456	CTCCATCAAGGTGTTCGACTTCAG---CGCTGGGCTGTGACAGCACGCGCCGAGCCGA	1512
Db	2528	CTCCATCAAGGCTTTTACTATGAAAGGCTTACAGCTGACGCGGCCCAATGACACGA	2587
QY	1513	CGCCGCGAGCGCCCTTACGACACCCCAACAGCTTCGCGATCAGTTTGGCAAGGCTGGGG	1572
Db	2588	GTTCATGCACACAAACCAATGAGAGCGGGTTCACCGGTGACAGATCAGTTTGAAGGCTGGGG	2647
QY	1573	GGCCTGTACATCCCGGAGATTTCATACACTCTCTGCCCTGTGTGGATGATCTCTCA	1637
Db	2648	CCAAGTCTACACCCGCAATTCATACGAGACTGCCGTGTGTGGAAGTATCTCAA	2707
QY	1633	CAACC 1637	
Db	2708	CAGCC 2712	
RESULT	13		
LOCUS	AF015260	1281 bp	21-OCT-1997
DEFINITION	Mus musculus Smad7 mRNA, complete cds.		
ACCESSION	AF015260		
KEYWORDS	92460039		
SOURCE	house mouse.		
ORGANISM	Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;		
REFERENCE	Rodentia; Sciurognathii; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 1281)		
	Nakao,A., Aitakhte,M., Moren,A., Nakayama,T., Christian,J.L.,		

FEATURES	source
TITLE	Heuchel, R., Itoh, S., Kawabata, M., Heldin, N.E., Heldin, C.H. and ten Dijke, P.
JOURNAL	Identification of Smad7, a TGFbeta-inducible antagonist of TGF-beta signaling
MEDLINE	Nature 389 (6651), 631-635 (1997)
REFERENCE	97474483
AUTHORS	2 (bases 1 to 1281) Nakao, A., Moran, A., Heuchel, R., Itoh, S., Heldin, C.-H. and ten Dijke, P.
TITLE	Direct Submission
JOURNAL	Submitted (21-JUL-1997) Ludwig Institute for Cancer Research, Uppsala Branch, Box 595, Biomedicine Center, Uppsala 75124, Sweden
source	Location/Qualifiers 1. 1281 /organism="Mus musculus" /db_xref="taxon:10090" 1. 1281 /note="TGF beta-induced signal response inhibitor" /codon_start=1 /product="Smad7" /db_xref="PID:g2460040" translation="MFRKRSALVRLMRSPAGCEDEEBCGGGGELRGEGATP GRATGAGGAGGAGRAGCCLIGRABGRGAKHHNHPPTSGAGAGAEADIKALTHVILKK LKEQDLLELLDAVSRSGRTACLLRGRIDCRGRPARAANOAPRSSSLPLLC KVFMRPDRHSSEYKRLCCCESTYKIRNELVCCPNHLSRCELESPPPSRIPMDL LKPPAGCPDAVPSSAETGGTNYLAPGGLSDQLLEPDRSHWCVAAWEKTRVGR YCSVEPSLIDFYDLDPQNGFCLIQVNDNSQLVQKVRSKIGCIGQLRVEDGVWYNN RSSPIRIFKATLDNPSRSLTGHKLVFNGPFGFIKAFDEKAYSLRPNDEHFMODPTWG FTVVISFVKGCCCTYRQFISSCCMCEVIINSN"
BASE COUNT	236 a 384 c 418 g 243 t
ORIGIN	

[illegible]

OY	856	CTTCACAGACCCGTGAGACTGAAGCCCTCTGGCGTGCACAAAGTTGGCCGCCGCC	915
Db	501	TCTTAGCATTCTCCGGAGAAGTCAAGAGGCTGTGGTGTAATCTTAGCGGAATCAA	560
OY	916	CGAGGGCCCTACCGGTGTGTGCAACCCTCATCACTTCAGCCGCTGTGGCGCCGATC	975
Db	561	CCCCGAC---TGTGTGTCTGCAACCCCTCACCTTAGTCGACTCTGTGAAGTCAAGTC	617
OY	976	TCCGCCACTTCCCCTACTCTCGGCTGTCTCCTCGGACGAGTACAAAGCCATGTATCTGC	1035
Db	618	TCCCCCTCTCTCTACTTCAG---ATAACCAATGATTTTCTCAAAACAACCTGGTGTCC	674
OY	1036	CGATTCACATTTGTTTACACTGAACGGAGGCTACCAATCCCTCATCACTCTCTCCGG	1095
Db	675	AGATGTGTACTCTTCTCCCTCGTGAAGCCGGGGGGAACAATTAATCT-----GGCCCTTG	728
OY	1096	TGAATTCACAGACCCGACATGTCTCCGAGCGCACCAACCCGACGCACTGTGTGACAGCT	1155
Db	729	GGGGCTTTCATATTCACACTTCTTCTTGAGCTCTGGGGATCCGCTACACTGTGTGTGT	788
OY	1156	GGCCTACTGGGAGCAGCCGACGCGCTGTGGCCCGCTCTATGCGGTGTACAGCAGGCGCT	1215
Db	789	GGCATCTGGGAGGAGAAGACGTGCGGTGGGAGGCTCTACTGTGTCCAAGGCCCTCCCT	848
OY	1216	CAGCATCTTCTAGCACTTACCTACAGGCGACGCGCTTCTGCTTGGCCAGCTCAACTGGA	1275
Db	849	GGATATCTTCTATGTATCTACTCTCAGGGGAATGGCTTTTGCTCTGGAGAGCTCAATTGCGA	908
OY	1276	GCACGCGACGCAATGCGGTGGCGGCGCAAGCGCAGCAAGATGGGTGGCATTCCTGTCAG	1335
Db	909	CAACAGAGTCAAGTGTGTGACAGAAAGTGGGAGCAAAATGTGGCTGTGTGATCCAGCTGAC	968
OY	1336	CAAGAGGCCCCAGCGCGTGTGGCCTCAACCCGCGGAGACCCCATCTTCTCAACTC	1395
Db	969	GGCGGAATGTGATGTGGCTGTGGTTTACAACCGAGCAGATTAACCCATCTTCAATCAAGTC	1028
OY	1396	CCCGACGCTGAGCGCGCCGCGGCGCCGCTGTGTGTGCGCAAGTGTCCCCCGGCTA	1455
Db	1029	CGCCCACTGTGAACAACCCGAGCTCAGGACGCTGTGTGTGACAAAATGTTTCCCTGTGT	1088
OY	1456	CTTCATCAAGTGTTCGACTTCGAG---CGTCTGGGCTGTGAGACGCGCCGAGCCCGA	1512
Db	1089	CTCCATCAAGGCTTTTGTACTGTGAGAAAGCTTACAGCTGTGAGGGCCCAATGACACGA	1148
OY	1513	CGCGCCGACGCGCCCTTCAGACCCCAACGAGGTCCGATAGCTTCGCCAAGGGCTGGG	1572
Db	1149	GTTCTATGCAAGCAACCATGTGAGGGGTTTTACCGGTGACATCAAGTTTGTGAAGGGCTGGG	1208
OY	1573	GCCCTGTACTTCCGCGCATTCATCACTCTCTGCCCTGTGTGCTGAGATCTCTCAA	1632
Db	1209	CCAGTGTACACCGCCGAGTTCATCAGCAGAGCTGCCCGGTGGCTGAGGATCATCTTCAA	1268
OY	1633	CAACC 1637	
Db	1269	CAGCG 1273	
RESULT 15			
LOCUS	AF010193	3111 bp mRNA	PRI 18-OCT-1997
DEFINITION	Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds.		
ACCESSION	AF010193		
NID	g2252821		
KEYWORDS	human.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;		
REFERENCE	Primates; Catarrhini; Hominoidea; Homo.		
AUTHORS	Hayashi,H., Abdollah,S., Qui,Y., Cai,J., Xu,Y.-Y., Grinnell,B.W., Jr.,		
	Richardson,M.A., Topper,J.N., Gimbrone,M.A. Jr., Wrana,J.L. and		
	Falsh,D.		
TITLE	The MAD-Related protein, Smad7, Associates with the TGF receptor		

[illegible]

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Db 864 ---TGGTGTCTGCAACCCCATCACCTTACCCACTCTGGAAGTCTAGAGTCTCCCCCC 920
QY 984 CTCCTACTCTGGCTGTCTCTCGGACGAGTACAAAGCCATGATCTGCGATTCCA 1043
Db 921 CTCCTACTCTGAGTACCCGATGATTTCTCAACCAACTGCAAGTCTCCAGATCTG 980
QY 1044 CATTGCTTACACTGAAGGAGGATACCAACTCCCTCATCTGCTCCGGTGAATCT 1103
Db 981 TGCCCTTCTCCGCTGAACAGGGGGAACGATATCT-----GGCCCTGGGGGCTTT 1034
QY 1104 CAGAGCCGCAATGTCTCCGACGCCACCAAGCCGACCTGCTGACCTGAGCTGCTACT 1163
Db 1035 CAGATTCCCAACTTCTTGGAGCTTGGGGATCGGACACTGCTGCTGCTGCTACT 1094
QY 1164 GGGACACCGGACGCGGCTGGGCTCTATGCGGTGTACGACGAGCCGCTCAGCATCT 1223
Db 1095 GGGAGGAGAAAGACGAGAGTGGGAGCTTACTGTCTCAGAGCCCTCTTGATATCT 1154
QY 1224 TCTACGACTTACTCAGGCGAGCGGCTTCTGCTGGGCCAGCTCAACCTGGAGCAGC 1283
Db 1155 TCTATGATCTACTCAGGGGAAATGCTTTTCTGCTGAGACACTCAATTCGACAACA 1214
QY 1284 GCGAGTGGGTGGCGGCAACCGGCAAGATCGGCTTGGCATCTGCTCAGCAAGAGC 1343
Db 1215 GTCAAGCTGTGTCAGAAAGTCCGGAGCAAAATCGGCTCGGCATCTCAGCTGAGCGG 1274
QY 1344 CCGAGCGCGTGTGGGCTTACACCGGCGAGCAGCAACCCATCTTCTGCACTCCCGAGC 1403
Db 1275 TGGATGTTGTGTGTGTACAAACCGCAGCATGTTACCCCATCTTCAATCAAGTCC 1334
QY 1404 TGGACCGCCCGCGCGCGGCTGCTGTGCGCAAGTGGCCCGGCTACTCCATCA 1463
Db 1335 TGGACAAACCGGACTCCAGAGCGCTTGTATACAAAGTGTCCCGGTTCTCATCA 1394
QY 1464 AGGTGTGACTTCAGGCTCTG---GGCTGACGACGCGCCGAGCCCGGAGCGCGCG 1520
Db 1395 AGGCTTTGACTACGAGAGGCTGACAGCTGACGCGCCCAATGACCAAGATTATGC 1454
QY 1521 AGGCGCCCTACGACCCCAACAGCGTCCGATCAGCTTGGCCAAAGGCTGGGGCCCTGCT 1580
Db 1455 AGCAGCGCTGAGCGGCTTTACCGTGCAGATCAGCTTGTGAAGGCTGGGGTCAGTCT 1514
QY 1581 ACTCCGCGACTTATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1637
Db 1515 ACACCCGCGAGTTCATCAGCAGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1571

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Search completed: May 4, 1999, 03:35:35
Job time: 2243 sec

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Apr 30 20:37:57 1999; Maspar time 39.28 Seconds

Tabular output not generated. 696.713 Million cell updates/sec

Title: >US-09-034-286-65
Description: (1-496) from US09034286.pep
Perfect Score: 3630
Sequence: 1 MFRSKRSLVRLMRSRVVP.....SROFINSCPWLEILLNPR 496

Scoring table:
PAM 150
Gap 11

Searched: 180763 segs, 55169189 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

sptrembl8
1:sp:archaea 2:sp:bacteria 3:sp:fungi 4:sp:human
5:sp:invertebrate 6:sp:mammal 7:sp:mhc 8:sp:organelle
9:sp:phage 10:sp:plant 11:sp:rodent 12:sp:unclassified
13:sp:vertebrate 14:sp:virus

Statistics: Mean 48.184; Variance 97.965; scale 0.492

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	3630	100.0	496	4	SMAD6.	0.00e+00
2	3627	99.9	496	4	SMAD6.	0.00e+00
3	3349	92.3	495	11	MAD HOMOLOG 7 (SMAD6).	0.00e+00
4	1646	45.3	235	4	SMAD6.	4.84e-303
5	1508	41.5	280	13	SMAD6 (FRAGMENT).	2.00e-274
6	1315	36.2	382	13	MAD-RELATED PROTEIN SM	1.51e-234
7	1293	35.6	382	13	SMAD7.	5.16e-230
8	1245	34.3	425	11	MAD-RELATED PROTEIN SM	3.92e-220
9	1242	34.2	425	4	MAD-RELATED GENE SMAD7	1.62e-219
10	1242	34.2	426	4	SMAD7 PROTEIN.	1.62e-219
11	1239	34.1	426	11	MAD HOMOLOG 8 (SMAD7).	6.72e-219
12	1219	33.6	425	11	SMAD7.	8.70e-215
13	515	14.2	568	5	DAD POLYPEPTIDE.	7.07e-73
14	363	10.0	467	13	MAD2.	7.73e-44
15	361	9.9	467	11	SMAD2 PROTEIN.	1.82e-43
16	361	9.9	467	4	JV18-1.	1.82e-43
17	361	9.9	467	11	MAD HOMOLOG 2 (MAD2).	1.82e-43
18	353	9.7	430	4	MOTHER AGAINST DPP (MA	5.61e-42
19	347	9.6	425	4	PROTEIN JV15-2 (DPP PR	7.31e-41
20	347	9.6	425	11	MOTHERS AGAINST DPP 3	7.31e-41

RESULT ID	1	PRELIMINARY:	PRT:	496 AA.
AC	043654;			
DT	01-JUN-1998 (TREMBLREL. 06, CREATED)			
DT	01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)			
DT	01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)			
DE	SMAD6.			
GN	SMAD6.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;			
CC	CATARRHINI; HOMINIDAE; HOMO.			
NC	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PLACENTA;			
RA	MOREN A.;			
RL	SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR	EMBL; AF043640; G2828712; -			
SQ	SEQUENCE 496 AA; 53497 MW; 310F8F08 CRC32;			

Query Match 100.0%; Score 3630; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 496; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	MFRSKRSLVRLMRSRVVPDREGGSGGGGDEGLSRAAPAPARREGGCGRSEV	60
Qy	1	MFRSKRSLVRLMRSRVVPDREGGSGGGGDEGLSRAAPAPARREGGCGRSEV	60
Db	61	RPVAPRRRDVAGRGAGARRRRAGPPRPAEPGAGASSLLDVAEPGPGWLPESD	120
Qy	61	RPVAPRRRDVAGRGAGARRRRAGPPRPAEPGAGASSLLDVAEPGPGWLPESD	120
Db	121	CETVCCGFSERDAAAGRADSDPLAGALPPAGGSRERERSLLEOLKTVYSL	180
Qy	121	CETVCCGFSERDAAAGRADSDPLAGALPPAGGSRERERSLLEOLKTVYSL	180
Db	181	KRLKRSIDLTLLEAVESRGVPGCVLPVRADRLGGGPAPPOLIGLRFMPDLOHAVE	240
Qy	181	KRLKRSIDLTLLEAVESRGVPGCVLPVRADRLGGGPAPPOLIGLRFMPDLOHAVE	240
Db	241	LKPLGCGSFAAADGPVCCNPHFSRLCGPESPYPYSLRSPRDEYKPLDSDSTLSY	300
Qy	241	LKPLGCGSFAAADGPVCCNPHFSRLCGPESPYPYSLRSPRDEYKPLDSDSTLSY	300
Db	301	TETETNSLITAPGFEFSASMSDATKPSHMCVSAWYEHRRVGRGLAVYDQAVSIFDL	360

Tue May 4 11:46:44 1999

US-09-034-286-65.rspt

Page 2

IMAPUR A ET AL

```

301 TETEAATNSLITAPGEFSDASMPDATKPSHMCVAYWEHRTVGRLAAYDQAVSIFYDL 360
361 POSGSGFCLGOLNLEORSESVRTRRSKIGFILLSKPEPDVWYVWYVNGEHPITFVNSPTLDAP 420
361 POSGSGFCLGOLNLEORSESVRTRRSKIGFILLSKPEPDVWYVWYVNGEHPITFVNSPTLDAP 420
421 GGRALVVRKVPYSGYSIKVDFEERSGLQHAPEPDADGPPYVNSVRSISFAKMGPCYSRQF 480
421 GGRALVVRKVPYSGYSIKVDFEERSGLQHAPEPDADGPPYVNSVRSISFAKMGPCYSRQF 480
481 ITSCPCWLEILLNPR 496
481 ITSCPCWLEILLNPR 496
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RESULT 2
AC 043541: PRELIMINARY: PRT: 496 AA.

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01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
SMAD6
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATAARRHINI; HOMINIDAE; HOMO.
[1]
SEQUENCE FROM N.A.
HARA A., LAGUNA G., MASSAGUE J., HEMMATI-BRIVANTLOU A.;
GENES DEV. 0:0-0(1997).
EMBL: AF035528; G2736316;
SEQUENCE 496 AA; 53496 MM; B0709066 CRC32;
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Query Match 99.9%; Score 3627; DB 4; Length 496;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 495; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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1 MFRSKRSGLVRLMRSRVPPVREGSGGGGGGDEDSLSGRAPAPARAREGGCGSRSEV 60
1 MFRSKRSGLVRLMRSRVPPVREGSGGGGGGDEDSLSGRAPAPARAREGGCGSRSEV 60
61 RPAVRRPRDPAVGRGAGGRRRRRAGGPPRPMSEPGAGSSLLDVAEPGGGWLPESD 120
61 RPAVRRPRDPAVGRGAGGRRRRRAGGPPRPMSEPGAGSSLLDVAEPGGGWLPESD 120
121 CEVTTCCLFSEERDAAGPRDASDPLAGALEPAGGGRSREARSRLILLEOELKTVYSL 180
121 CEVTTCCLFSEERDAAGPRDASDPLAGALEPAGGGRSREARSRLILLEOELKTVYSL 180
121 CEVTTCCLFSEERDAAGPRDASDPLAGALEPAGGGRSREARSRLILLEOELKTVYSL 180
181 KRLKERSLDITLLEAVESRGVPGGCVLPBRADLRGGQAPAPOLLGRLFRMPDLOHAVE 240
181 KRLKERSLDITLLEAVESRGVPGGCVLPBRADLRGGQAPAPOLLGRLFRMPDLOHAVE 240
181 KRLKERSLDITLLEAVESRGVPGGCVLPBRADLRGGQAPAPOLLGRLFRMPDLOHAVE 240
241 LKPLCGCHSFAAADGPTVCNPFHFSRLCGPESPPPYRSLSPEDYKPLDLSDSL 300
241 LKPLCGCHSFAAADGPTVCNPFHFSRLCGPESPPPYRSLSPEDYKPLDLSDSL 300
241 LKPLCGCHSFAAADGPTVCNPFHFSRLCGPESPPPYRSLSPEDYKPLDLSDSL 300
301 TETEAATNSLITAPGEFSDASMPDATKPSHMCVAYWEHRTVGRLAAYDQAVSIFYDL 360
301 TETEAATNSLITAPGEFSDASMPDATKPSHMCVAYWEHRTVGRLAAYDQAVSIFYDL 360
361 POSGSGFCLGOLNLEORSESVRTRRSKIGFILLSKPEPDVWYVWYVNGEHPITFVNSPTLDAP 420
361 POSGSGFCLGOLNLEORSESVRTRRSKIGFILLSKPEPDVWYVWYVNGEHPITFVNSPTLDAP 420
421 GGRALVVRKVPYSGYSIKVDFEERSGLQHAPEPDADGPPYVNSVRSISFAKMGPCYSRQF 480
421 GGRALVVRKVPYSGYSIKVDFEERSGLQHAPEPDADGPPYVNSVRSISFAKMGPCYSRQF 480
481 ITSCPCWLEILLNPR 496
481 ITSCPCWLEILLNPR 496
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301 TETEAATNSLITAPGEFSDASMPDATKPSHMCVAYWEHRTVGRLAAYDQAVSIFYDL 360
361 POSGSGFCLGOLNLEORSESVRTRRSKIGFILLSKPEPDVWYVWYVNGEHPITFVNSPTLDAP 420
361 POSGSGFCLGOLNLEORSESVRTRRSKIGFILLSKPEPDVWYVWYVNGEHPITFVNSPTLDAP 420
421 GGRALVVRKVPYSGYSIKVDFEERSGLQHAPEPDADGPPYVNSVRSISFAKMGPCYSRQF 480
421 GGRALVVRKVPYSGYSIKVDFEERSGLQHAPEPDADGPPYVNSVRSISFAKMGPCYSRQF 480
481 ITSCPCWLEILLNPR 495
481 ITSCPCWLEILLNPR 495
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RESULT 3
AC 035182: PRELIMINARY: PRT: 495 AA.

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01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
MAD6
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIOGROGNAHI; MURIDAE; MURINAE; MUS.
[1]
SEQUENCE FROM N.A.
MEDLINE: 97474481.
RA IMAMURA T., TAKASE M., NISHIHARA A., OEDA E., HANAI J.-I., KAMABATA M.,
RA "Smad6 inhibits signalling by the TGF-beta superfamily."
RL NATURE 389:622-626(1997).
DR EMBL: AF010133; G2507640;
DR MGD: MGI:1100516; MAD6.
PRIM: PF00968; Dwaifin; 1.
SEQUENCE 495 AA; 53714 MM; 0C0B42D1 CRC32;
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Query Match 92.3%; Score 3349; DB 11; Length 495;
Best Local Similarity 93.0%; Pred. No. 0.00e+00;
Matches 463; Conservative 14; Mismatches 16; Indels 5; Gaps 4;

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61 RPAVRRPRDPAVGRGAGGRRRRRAGGPPRPMSEPGAGSSLLDVAEPGGGWLPESD 120
61 RPAVRRPRDPAVGRGAGGRRRRRAGGPPRPMSEPGAGSSLLDVAEPGGGWLPESD 120
120 CEVTTCCLFSEERDAAGPRDASDPLAGALEPAGGGRSREARSRLILLEOELKTVYSL 179
120 CEVTTCCLFSEERDAAGPRDASDPLAGALEPAGGGRSREARSRLILLEOELKTVYSL 179
121 CEVTTCCLFSEERDAAGPRDASDPLAGALEPAGGGRSREARSRLILLEOELKTVYSL 178
180 LKRLKERSLDITLLEAVESRGVPGGCVLPBRADLRGGQAPAPOLLGRLFRMPDLOHAVE 239
180 LKRLKERSLDITLLEAVESRGVPGGCVLPBRADLRGGQAPAPOLLGRLFRMPDLOHAVE 239
179 LKRLKERSLDITLLEAVESRGVPGGCVLPBRADLRGGQAPAPOLLGRLFRMPDLOHAVE 238
240 VELKPLCGCHSFAAADGPTVCNPFHFSRLCGPESPPPYRSLSPEDYKPLDLSDSL 299
240 VELKPLCGCHSFAAADGPTVCNPFHFSRLCGPESPPPYRSLSPEDYKPLDLSDSL 299
239 VELKPLCGCHSFAAADGPTVCNPFHFSRLCGPESPPPYRSLSPEDYKPLDLSDSL 298
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299 SYTETATNSLITAPGEFSDASMPDATKPSHMCVAYWEHRTVGRLAAYDQAVSIFYDL 358
360 DEPOSGSGFCLGOLNLEORSESVRTRRSKIGFILLSKPEPDVWYVWYVNGEHPITFVNSPTLDAP 419
360 DEPOSGSGFCLGOLNLEORSESVRTRRSKIGFILLSKPEPDVWYVWYVNGEHPITFVNSPTLDAP 419
359 DEPOSGSGFCLGOLNLEORSESVRTRRSKIGFILLSKPEPDVWYVWYVNGEHPITFVNSPTLDAP 418
420 GGRALVVRKVPYSGYSIKVDFEERSGLQHAPEPDADGPPYVNSVRSISFAKMGPCYSR 477
420 GGRALVVRKVPYSGYSIKVDFEERSGLQHAPEPDADGPPYVNSVRSISFAKMGPCYSR 477
419 GGRALVVRKVPYSGYSIKVDFEERSGLQHAPEPDADGPPYVNSVRSISFAKMGPCYSR 478
478 GGRALVVRKVPYSGYSIKVDFEERSGLQHAPEPDADGPPYVNSVRSISFAKMGPCYSR 478
479 OPTSCPCWLEILLNPR 495
479 OPTSCPCWLEILLNPR 495
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RESULT 4
AC 015799: PRELIMINARY: PRT: 235 AA.

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01-NOV-1996 (TREMBLREL. 01, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
SMAD6.
HOMO SAPIENS (HUMAN).
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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CAVARHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96259564.
RA RIGGINS G.J., THIAIALINGAM S., ROZENBLUM E., WEINSTEIN C.L., KERN S.E.,
RA HAMILTON S.R., WILSON J.K., MARKOWITZ S.D., KINZLER K.W.,
RA VOGELSTEIN B.;
RT "Mad-related genes in the human.";
RL NAT. GENET. 13:347-349(1996).
DR EMBL; U59914; G1654327; -
DR PIRAM; PF00968; Dwarfin; 1.
SQ SEQUENCE 235 AA; 26235 MW; F696E2F2 CRC32;

Query Match 45.3%; Score 1646; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 4,84e-303;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 13 SPPEYSLSPRDEKPLDLSSTLYETETATNSLITAPGEFSDASMPDAPKPSHMS 72
OY |||||||
DB 274 SPPEYSLSPRDEKPLDLSSTLYETETATNSLITAPGEFSDASMPDAPKPSHMS 333
OY |||||||
DB 73 VAYWEHRTVGRILAVYDOAVSIFDLPQSGGFCGLQNLQORSVARTSKIGFILL 132
OY |||||||
DB 334 VAYWEHRTVGRILAVYDOAVSIFDLPQSGGFCGLQNLQORSVARTSKIGFILL 393
OY |||||||
DB 133 SKEPQVAYNRGEHPIFVNSPTLDAPGGRALVYKVPYSGIKYFDEERSGLOHAPED 192
OY |||||||
DB 394 SKEPQVAYNRGEHPIFVNSPTLDAPGGRALVYKVPYSGIKYFDEERSGLOHAPED 453
OY |||||||
DB 193 AADPYDPSVYRISFAKMGPCYSROFTSCPCWLEILLNPR 235
OY |||||||
DB 454 AADPYDPSVYRISFAKMGPCYSROFTSCPCWLEILLNPR 496
OY |||||||

RESULT 5 PRELIMINARY; PRT; 280 AA.
ID 057475;
AC 057475;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE SMAD6 (FRAGMENT).
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
OC MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENODIDINAE; XENOPUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-HEAD;
RA HATA A., LAGNA G., MASSAGUE J., HEMMATI-BRIVANDOU A.;
RL GENES DEV. 0:0-0(1997).
DR EMBL; AF055529; G2736318; -
FT NON_TER 1
SQ SEQUENCE 280 AA; 31094 MW; 685518EF CRC32;

Query Match 41.5%; Score 1508; DB 13; Length 280;
Best Local Similarity 70.5%; Pred. No. 2,00e-274;
Matches 196; Conservative 45; Mismatches 31; Indels 6; Gaps 4;

DB 4 HGPRLHLLCLFRLPELQHPQQLKALSGCQAGSDNNGCCCNPHYSHVCEPESP 63
OY :|||||
DB 218 QPAPQLLGLRFLRMPDLQHVELKPLCGCHSFAAADGPTVCC-NPYHFSRLCPESP 276
OY |||||||
DB 64 PPSYLSKIKQKPLDLSDS--YTEMASNSLCTIADISTSLSPMSKQGHWCYAY 120
OY |||||||
DB 277 PPSYLSKIKQKPLDLSDS--YTEMASNSLCTIADISTSLSPMSKQGHWCYAY 336
OY |||||||
DB 121 WEHRRVRLVAVCPSYIFDLPQSGGFCGLQNLQORSVARTSKIGFILL 180
OY |||||||
DB 337 WEHRRVRLVAVCPSYIFDLPQSGGFCGLQNLQORSVARTSKIGFILL 396
OY |||||||
DB 181 TDGVAYNRSDHPIFVNSPTLDAPGGRALVYKVPYSGIKYFDEERSGLOHAPED 240
OY |||||||
DB 397 TDGVAYNRSDHPIFVNSPTLDAPGGRALVYKVPYSGIKYFDEERSGLOHAPED 454
OY |||||||

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DB 241 TDGPYDPSVYRISFAKMGPCYSROFTSCPCWLEILL 278
OY :|||||
DB 455 ADGPYDPSVYRISFAKMGPCYSROFTSCPCWLEILL 492
OY :|||||

RESULT 6 PRELIMINARY; PRT; 382 AA.
ID 057459;
AC 057459;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SMAD7.
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
OC MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENODIDINAE; XENOPUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98119796.
RA NAKAYAMA T., SNYDER M.A., GREML S.S., TSUNEIZUMI K., TABATA T.,
RA CHRISTIAN J.L.;
RT "Xenopus Smad8 acts downstream of BMP-4 to modulate its activity
RT during vertebrate embryonic patterning.";
RL DEVELOPMENT 125:857-867(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA BHUSHAN A., CHEN Y., VALE W.;
RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF026125; G3158344; -
DR EMBL; AF045742; G3005093; -
SQ SEQUENCE 382 AA; 42713 MW; 22E791D CRC32;

Query Match 36.2%; Score 1315; DB 13; Length 382;
Best Local Similarity 53.0%; Pred. No. 1.51e-234;
Matches 174; Conservative 71; Mismatches 75; Indels 8; Gaps 6;

DB 58 ELKALAHCVLKKLEKQLEGILQAVECKGARGSCILLPAKLDLSRGOAFSLPLICK 117
OY |||||||
DB 171 ELKTYSLKRLKRLERSLDTLEAVESRGVPGGCVLVRDL--RLGQAPQOLLGR 228
OY |||||||
DB 118 VFRPDLRHSVDVRLSCDSYGRN-NPELLCCNPHLSRLCELESPPPYTRY-PMDFL 175
OY :|||||
DB 229 LFRPDLQHVELKPLCGCHSFAAADGPTVCCNPHYHSLRCLGESPSPYSLSPRDEY 288
OY |||||||
DB 176 KPLADSPSVSSSTETGTNL--APEGLDSQLLHETGDSHNCMAVWEKTRVGRLY 233
OY |||||||
DB 289 KPL-DLSDSTLYETETATNSLITAPGEFSDASMPDAPKPSHMSVAYWEHRTVGRLY 347
OY |||||||
DB 234 SVQPSLDIFDLPQSGGFCGLQNLQORSVARTSKIGFILLQREVDGVWYVNRSS 293
OY :|||||
DB 348 AVYDOAVSIFDLPQSGGFCGLQNLQORSVARTSKIGFILLQREVDGVWYVNRSS 407
OY |||||||
DB 294 YPIFKSATLDPDPSRLTLVHKVPEGSIKAFDEKAYSLQRPNDHEFMQPMGTVOI 353
OY |||||||
DB 408 HPIFVNSPTLDAPGGRALVYKVPYSGIKYFDEERSGLOHAPEDPADGPYDPSVRI 466
OY |||||||
DB 354 SFVKGWGCCTYRQFISSCPCWLEIYFNN 381
OY |||||||
DB 467 SFVKGWGCCTYRQFISSCPCWLEIYFNN 494
OY |||||||

RESULT 7 PRELIMINARY; PRT; 382 AA.
ID 057522;
AC 057522;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE SMAD7.
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
OC MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENODIDINAE; XENOPUS.
RN [1]

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RP SEQUENCE FROM N.A.
RA CASSELLAS R., HEMMATI-BRIVANLOU A.;
DR SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RL EMBL: AF042198; G2921581;
SQ SEQUENCE 382 AA; 42729 MW; 653E5184 CRC32;

Query Match 35.6%; Score 1293; DB 13; Length 382;
Best Local Similarity 52.4%; Pred. No. 5,16e-230;
Matches 172; Conservative 70; Mismatches 78; Indels 8; Gaps 6;

Db 58 QKALAHCVLEELKEKOLEGLQAVECKGASPCOLLPAKIDSLGQAFSLPLICK 117
Y 171 ELKVTYSILKRLKERSIDTLLAEVSRGCVGCVLRADL--RLGGQAPAPOLLICR 228
Db 118 VERMPDLRSHSDVKRLSCDSYGRN-NPELLCCNPHHSRLCELESPPPYTRY-PMFL 175
Y 229 LFRWMDLOHAEVLKLCCHSPAAADGPYVCNPFHFSRLCGPSPPPYRSLSPRDEY 288
Db 176 KPLADSPDVPSSSETGTGTFNLA-APEGLSDSLHETGDPHWMQVAYWEKTVGRLY 233
Y 289 KPL-DLSDSTLYTETATNSLITAPGEFSDASMPDATKFSHMCVAYWEHRTVRGLY 347
Db 234 SVQPSLDFIDLPQNGFCGLQNSDNKSQLVOKVRKISGIGIOLTKREVGVWYNNSS 293
Y 348 AVYQAVSIFDLPQSGFCGLQNLLEQSRSESVRTRSKIGFILLSKRPGVAYNNGE 407
Db 294 YPIFKSATLNDPDSRTLLVHKVPGFSIKAFDEKAYSLORLNDHEFMQPTGTVOI 353
Y 408 HPIVNSPTLDAPGGRALVAKVPVPSIKVDFERS-GLQHAEPDADGPDPNSVRI 466
Db 354 SEYKMGOCYCTROFISSCPCWLEVIENN 381
Y 467 SFAKMGPCYSROFITSCPCWLEILLNN 494

RESULT 8 PRELIMINARY; PRT; 425 AA.

ID 088709; AC 088709; DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE MAD-RELATED PROTEIN SMAD7B.
GN SMAD7B.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
NC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
[1]
SEQUENCE FROM N.A.
RC TISSUE-WHOLE EMBRYOS;
RA KITAMURA K., OKAZAKI K.;
RT "Isolation of cDNAs encoding mouse homologues of Mad (Smad7 and
RT Smad7B) that can mediate TGF-beta family signalling."
RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AJ000551; E1313655;
FT VARIANT 232 232 V -> A (IN REF. 1).
SQ SEQUENCE 425 AA; 46398 MW; 4EBCDE29 CRC32;

Query Match 34.3%; Score 1245; DB 11; Length 425;
Best Local Similarity 53.8%; Pred. No. 3.92e-220;
Matches 183; Conservative 65; Mismatches 74; Indels 18; Gaps 9;

Db 89 EADKALHSHVILKRLKEROLELLQAVESRGSTRACLLPRLDRCRGLGAPASAPQAQ 148
Y 169 EQLKTVYSLKRLKERSLDTLLAEVSRGCVGCVLP-RADLRIG-G----QPA- 220
Db 149 PPSYSILPLICKVFRWDLRHSSEVKRLCCESYGI-NPELVCCNPHHSRLCELSPP 207
Y 221 PP-----QLLGRLEFRWDLQHAVELKPLCGCHSPAAADGPYVCNPFHFSRLCGPSP 275
Db 208 PPSYSR-PMFLKPTGCPDAVPSSVETGTNYL--APGLSDSLLEPDRSHMCVYA 264
Y 276 PPSYRSLSPRDEYKPLDLSSTLYTETATNSLITAPGEFSDASMSDPDATKFSHMCVYA 335

Db 265 YWEKTRVGRLYCYOEPSLDFYDLPOGNGFCLQNSDNKSQLVOKVRKISGIGIOLTR 324
Y 336 YWEHRTVRGLALVADQAVSYTDLDPQSGFCGLQNLLEQSRSESVRTRSKIGFILLSK 395
Db 325 EVDGVWYNNSSPIPIFKSATLNDPDSRTLLVHKVPGFSIKAFDEKAYSLORNDHEF 384
Y 396 EPDGVWYNNRGRHPIFVNSPTLDAPGGRALVAKVPVPSIKVDFERS-GLQHAEPDPA 454
Db 385 MQQPTGTVOISFVKMGOCYCTROFISSCPCWLEVIENN 424
Y 455 ADGPYDPNSVRI SFAKMGPCYSROFITSCPCWLEILLNN 494

RESULT 9 PRELIMINARY; PRT; 426 AA.

ID 015105; AC 015105; DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE MAD-RELATED GENE SMAD7.
GN SMAD7.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
NC CATARRHINI; HOMINIDAE; HOMO.
[1]
SEQUENCE FROM N.A.
RA HAYASHI H., ABDOLLAH S., QUT Y., CAI J., XU Y.-Y., GRINNELL B.W.,
RA RICHARDSON M.A., TOPPER J.N., GIMBRONE M.A. JR., WRANA J.L., FALB D.,
RL CELL 0:0-0(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97404392.
RA TOPPER J.N., CAI J., QUT Y., ANDERSON K.R., XU Y.-Y., DEEDS J.D.,
RA FEELY R., GIMBRONE M.A. JR., FALB D.,
RA SCHOEN F.J., GIMBRONE M.A. JR., FALB D.;
RT "Vascular MADS: two novel MAD-related genes selectively inducible by
RT flow in human vascular endothelium."
RL PROC. NATL. ACAD. SCI. U.S.A. 94:9314-9319(1997).
DR EMBL: AF010193; G2252822;
DR PRAM: PF00968; Dwaflin; 1.
SQ SEQUENCE 426 AA; 46425 MW; 598F0022 CRC32;

Query Match 34.2%; Score 1242; DB 4; Length 426;
Best Local Similarity 54.0%; Pred. No. 1.62e-219;
Matches 184; Conservative 66; Mismatches 72; Indels 19; Gaps 10;

Db 89 EADKALHSHVILKRLKEROLELLQAVESRGSTRACLLPRLDRCRGLGAPASAPQAQ 148
Y 169 EQLKTVYSLKRLKERSLDTLLAEVSRGCVGCVLP-RADLRIG-G----QPA- 220
Db 149 PPSYSILPLICKVFRWDLRHSSEVKRLCCESYGI-NPELVCCNPHHSRLCELSPP 207
Y 221 PP-----QLLGRLEFRWDLQHAVELKPLCGCHSPAAADGPYVCNPFHFSRLCGPSP 275
Db 208 PPSYSR-PMFLKPTGCPDAVPSSVETGTNYL--APGLSDSLLEPDRSHMCVYA 264
Y 276 PPSYRSLSPRDEYKPL-DLSSTLYTETATNSLITAPGEFSDASMSDPDATKFSHMCV 334
Db 265 AYWEKTRVGRLYCYOEPSLDFYDLPOGNGFCLQNSDNKSQLVOKVRKISGIGIOLTR 324
Y 336 YWEHRTVRGLALVADQAVSYTDLDPQSGFCGLQNLLEQSRSESVRTRSKIGFILLSK 395
Db 325 EVDGVWYNNSSPIPIFKSATLNDPDSRTLLVHKVPGFSIKAFDEKAYSLORNDHEF 384
Y 396 EPDGVWYNNRGRHPIFVNSPTLDAPGGRALVAKVPVPSIKVDFERS-GLQHAEPDPA 454
Db 385 MQQPTGTVOISFVKMGOCYCTROFISSCPCWLEVIENN 425
Y 454 AADGPYDPNSVRI SFAKMGPCYSROFITSCPCWLEILLNN 494

RESULT 10 PRELIMINARY; PRT; 426 AA.
ID 014740

[illegible]

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RA KITAMIR.K., OKAZAKI.K.;
RT "Characterization of a novel mouse homologue of Mad, Smad7, that can
RL mediate TGF-beta family signalling.";
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF015260; G2460040; -
DR EMBL: AJ000550; E113653; -
DR MGI: MGI:1100524; MADH8.
DR PPM; PF00968; Dwarfin; 1.
SQ SEQUENCE 426 AA; 46441 MW; 61CE1D5B CRC32;

Query Match 34.1%; Score 1239; DB 11; Length 426;
Best Local Similarity 53.7%; Pred. No. 6,72e-219;
Matches 183; Conservative 66; Mismatches 73; Indels 19; Gaps 10;

Db 89 EADLKALTHSVLKIKERQLELLIQAVESRGCTRTACLLPGLRDLRGAPASAPAO 148
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Oy EQELKTVYSLIKRLKERSLDLTLEAVESRGVGCGVLVP-RADRLIG-G-----QPA- 220

Db 149 PPSVSLPILLCVFRPMDLRHSEVVKRLCCCEYKGI-NPELVCCNPHLSRLCELESP 207
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Oy 221 PP-----QLLGRLEFRPMDLOHAEVLRPLCGCHSFAAAGPTVCCNPHYSRLCGPESP 275

Db 208 PPEYSRY-PMDFLKPFGAGCPDAVSSAETGNTLV--APGGLSDSOLLPEPGRSHWCYV 264
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Oy 276 PPEYSRLSPRDEYRPDL-SDSTLSYTEETATNSLITRAPEFSDASMPATRPSHMCV 334

Db 265 AYWEKTRVGRVLYCQVEPSLIDIFYDLPGNGFCGLQLNSDNKSQLYOKVRSKIGCGIQLT 324
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Oy 335 AYWEHRTVRGRVLYAVDQAVSIFDLPDQSGSGFCGLQNTLEQRESVVRTRSKIGGILLS 394

Db 325 REVQGVWYVNNSSPIPIKSLTLDNPSRLLVHKVPPGSIKAFDEKAYSLQRPDHE 384
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Oy 395 KEPDQVWYVNNSEHPIFNSPTLDAPGRALVYAKVPBGYSIKVFERS-GLQHAPEPD 453

Db 385 FMOQEPMTGFTVOISPFVKMGCCYTRPFSSPCPCWLEVIIFS 425
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Oy 454 AADGPYDENSVRISFAKMGPCYSROFITSCPHLEILLNN 494

RESULT 12 PRELIMINARY; PRT; 425 AA.
ID 088406
AC 088406;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DI SMAD7.
OS RATTUS NORVEGICUS (RAT).
OC EUTARVOTA; METAOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCUROGNATHI; MORIDAE; MURINAE; RATTUS.
RN (1)
RP SEQUENCE FROM N.A.
RA CHEN Y., VALE W.;
RT "Inhibition of activin signaling by Smad7.";
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF042499; G3282769; -
SQ SEQUENCE 425 AA; 46354 MW; F41D6DBB CRC32;

Query Match 33.6%; Score 1219; DB 11; Length 425;
Best Local Similarity 53.7%; Pred. No. 8.70e-215;
Matches 183; Conservative 66; Mismatches 72; Indels 20; Gaps 11;

Db 89 EADLKALTHSVLKIKERQLELLIQAVESRGCTRTACLLPGLRDLRGAPASAPAO 148
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Oy 169 EQELKTVYSLIKRLKERSLDLTLEAVESRGVGCGVLVP-RADRLIG-G-----QPA- 220

Db 149 PPSVSLPILLCVFRPMDLRHSSVVKRLCCCEYKGI-N-PELVCCNPHLSRLCELESP 206
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Oy 221 PP-----QLLGRLEFRPMDLOHAEVLRPLCGCHSFAAAGPTVCCNPHYSRLCGPESP 275

Db 207 PPEYSRY-PMDFLKPFGAGCPDAVSSDTEGTNTLV--APGGLSDSOLLPEPGRSHWCYV 263
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Oy 276 PPEYSRLSPRDEYKRL-DLSDSLSTYETATNSLITRAPEFSDASMSPDATKRSIMCV 334

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Db 264 AYWEKTRVGRGLYCVQEPDIDFYDLPOGNGFCGLGOLNSDNKSLVQKVNSTIGCGTOLT 323
 QY 335 AYWEHRTVRGLYAVYQGANISIFDLQGGSGFCGLGOLNLSRSESVRTRKSTIGCGTOLT 394
 Db 324 REVDGVAWVYRSTYPIFKATLNDPDSRLLVHVKVPGFSIAFDEKXYSIORPDHE 363
 QY 395 KEPDGVAWVYRSTYPIFKATLNDPDSRLLVHVKVPGFSIAFDEKXYSIORPDHE 393
 Db 384 FMOQPTGFTVYQSFVKGWGCCTROFISCPWLEVIENS 424
 QY 454 AADGPDVNSVSRISFAKMGPCYSRQFITSQPCWLEILLNN 494

RESULT 13
 ID 015968 PRELIMINARY: PRT: 568 AA.
 AC 015968:
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE DAD POLYPEPTIDE.
 OS DROSOPHILA MELANOGASTER (FRUIT FLY).
 CC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
 CC PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYROIDEA;
 CC DROSOPHILIDAE; DROSOPHILA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97474482.
 RA TSUNETSUMI K., NAKAYAMA T., KAMOSHIDA Y., KORBERG T.B.,
 RA CHRISTIAN J.L., TABATA T.,
 RT "Daughters against dpp modulates dpp organizing activity in Drosophila
 wing development."
 RL NATURE 389:627-631(1997).
 DR EMBL: AB004232; D1023711;
 PRFAM: PF00968; Dwaflin; 1.
 SQ SEQUENCE 568 AA; 63605 MW; B414441E CRC32;

Query Match 14.2%; Score 515; DB 5; Length 568;
 Best Local Similarity 38.4%; Pred. No. 7,07e-73;
 Matches 113; Conservative 51; Mismatches 105; Indels 25; Gaps 18;

Db 281 PHYTASRLFWRELWNAKELKRLPTC---PAARDCIYMCNPLHMFRLHQEPESPTTP 337
 QY 222 POLLRLEFLFMPDLQHAYELKPLCGHSFAAADGPRVCNPH-FSRLGPE--SPPP 278
 Db 338 YQSKMLRLKADAEDESDQDAKSAISTASSTISNLYKALYESVTTDKDNHNS 397
 279 Y--SR-LSPRD-EYK--PL-DLSDSTLYTETATN-SLTITAGFSDAMSP-DATKPS 329
 Db 398 QVWCQIAYWEMARVGEFEFAKTNVAVITDGIYASEVDSMCLADITPAGNOIHVVPTA 457
 QY 330 H-WCSVAWYEHRTVRGLYAVYQGANISIFD--POGSGFCGLGOLNLSRSESVRTR 383
 Db 458 RTTVGIGVLTSLNGDVTWYNGNTTIFVDSPTLSENLR--VC-KVMGYCKAETNR 514
 QY 384 REKIFGILLKEPDCGVMAVYNGEHPFVNSPTLDAPGRALVYKVPYSGISIKVFDEFR 443
 Db 515 AELLMBRDGHHPMPVYFSIKISFGKMGWGRDYKRODIMGCPWLEVHSLR 568
 QY 444 SGLQHAPEPDA-ADGPDVNSVSRISFAKMGPCYSRQFITSQPCWLEILLNNPR 496

RESULT 14
 ID 091912 PRELIMINARY: PRT: 467 AA.
 AC 091912:
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE MAD2.
 GN MAD2.
 OS XENOPUS LAEVIS (AFRICAN CLAMMED FROG).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
 CC MESOBATRACHIA; PIPOIDEA; PIPOIDAE; XENODIDINAE; XENOPUS.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE: 96222291.
 RA GRAFF J.M., BANSAL A., MELTON D.A.;
 RT "Xenopus Mad proteins transduce distinct subsets of signals for the
 RT TGF beta superfamily."
 RL CELL 85:479-487(1996).
 DR EMBL: L77885; G1333645;
 PRFAM: PF00968; Dwaflin; 1.
 SQ SEQUENCE 467 AA; 52411 MW; 1245ED6E CRC32;

Query Match 10.0%; Score 363; DB 13; Length 467;
 Best Local Similarity 32.3%; Pred. No. 7,73e-44;
 Matches 75; Conservative 57; Mismatches 88; Indels 12; Gaps 9;

Db 218 PETPPPGY--ISEDETSQDQNSMDTGSFPAELSPSTLS-PVN-HNLDQPYTSEPAF 273
 QY 272 PESPPPPYRSLSPRDEYKPLDSDSTLYTETATNSLITAPGFSDSMSPDATKPSH 330
 Db 274 WCSIAYVELNQRVGETHFASQPSLTVDGFTDPSNSERFCLLSNVNNAVTVMTRRHIG 333
 QY 331 WCSIAYVELNQRVGETHFASQPSLTVDGFTDPSNSERFCLLSNVNNAVTVMTRRHIG 338
 Db 334 RGVRLYYIGEVFAECSDSAIFVQSPNCNRYGMHPATYCKIPGCKLTFNNOEPAAL 393
 QY 389 FGILLSKEPDGVMAVYNGEHPFVNSPTLDAPGR-ALVYKVPYSGISIKVFDEFR-SGL 446
 Db 394 LAQSVNQGFEAVYQLTFRCTIRMSFVKGWGAERYRQTYTSPCWLIELHNP 445
 QY 447 QHAPEPDAADPDV-PN-SVSRISFAKMGPCYSRQFITSQPCWLEILLNNPR 495

RESULT 15
 ID 070436 PRELIMINARY: PRT: 467 AA.
 AC 070436:
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE SMAD2 PROTEIN.
 GN SMAD2.
 OS RATTUS NORVEGICUS (RAT).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 CC SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA OSAKI M., YONEKURA A., MIYAZAKI Y., HIROTA Y., ONO N., SONTA S.,
 RA NAKA H., OHTSUKA A., TSUKAZAKI T., SHINDO H., YAMASHITA S.,
 RA SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
 RA ZHANG Y.-Q., KANZAKI M., KOJIMA I.;
 RT "Rat Smad2."
 RL SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF056001; G3025890;
 DR EMBL: AB017912; D1034419;
 SQ SEQUENCE 467 AA; 52239 MW; FD9EFE07 CRC32;

Query Match 9.9%; Score 361; DB 11; Length 467;
 Best Local Similarity 32.3%; Pred. No. 1,82e-43;
 Matches 75; Conservative 57; Mismatches 88; Indels 12; Gaps 9;

Db 218 PETPPPGY--ISEDETSQDQNSMDTGSFPAELSPSTLS-PVNS-LDQPYTSEPAF 273
 QY 272 PESPPPPYRSLSPRDEYKPLDSDSTLYTETATNSLITAPGFSDSMSPDATKPSH 330
 Db 274 WCSIAYVELNQRVGETHFASQPSLTVDGFTDPSNSERFCLLSNVNNAVTVMTRRHIG 333
 QY 331 WCSIAYVELNQRVGETHFASQPSLTVDGFTDPSNSERFCLLSNVNNAVTVMTRRHIG 338
 Db 334 RGVRLYYIGEVFAECSDSAIFVQSPNCNRYGMHPATYCKIPGCKLTFNNOEPAAL 393
 QY 389 FGILLSKEPDGVMAVYNGEHPFVNSPTLDAPGR-ALVYKVPYSGISIKVFDEFR-SGL 446

Tue May 4 11:46:44 1999

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Page 7

D_b 394 IASVNOGEAVYQLTIRMCTIRNSFYKGMGAERKROVTSTPNCIEHLNCP 445
 : :: : |::| |||| : | : || ||| : | |
QY 447 CHAPPDADGPD-DN-SVRISFAKMGPCYSRQRTTSCPCWLEILLNNP 495

Search completed: Fri Apr 30 20:39:41 1999
Job time : 104 secs.

